

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/501, 671 A  
Source: PCT  
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## RAW SEQUENCE LISTING

DATE: 11/10/2005

PATENT APPLICATION: US/10/501,671A

TIME: 09:10:46

Input Set : A:\80621021.app

Output Set: N:\CRF4\11102005\J501671A.raw

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3 <110> APPLICANT: NISHIO, FUMIHIDE
5 <120> TITLE OF INVENTION: HIGH-CONCENTRATION PREPARATION OF SOLUBLE
6   THROMBOMODULIN
8 <130> FILE REFERENCE: 8062-1023
10 <140> CURRENT APPLICATION NUMBER: 10/501,671A
11 <141> CURRENT FILING DATE: 2004-07-16
13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00339
14 <151> PRIOR FILING DATE: 2003-01-17
16 <150> PRIOR APPLICATION NUMBER: JP2002-9951
17 <151> PRIOR FILING DATE: 2002-01-18
19 <160> NUMBER OF SEQ ID NOS: 9
21 <170> SOFTWARE: PatentIn Ver. 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 516
25 <212> TYPE: PRT
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial amino
30   acid sequence of human-originated soluble
31   thrombomodulin
33 <400> SEQUENCE: 1
34 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
35   1           5           10           15
37 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
38   20           25           30
40 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
41   35           40           45
43 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
44   50           55           60
46 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
47   65           70           75           80
49 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
50   85           90           95
52 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
53   100          105          110
55 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
56   115          120          125
58 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
59   130          135          140
61 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
62   145          150          155          160
64 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
65   165          170          175

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67 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Val Ser Ile Thr
68           180           185           190
70 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
71           195           200           205
73 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
74           210           215           220
76 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
77 225           230           235           240
79 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
80           245           250           255
82 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
83           260           265           270
85 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
86           275           280           285
88 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
89           290           295           300
91 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
92 305           310           315           320
94 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
95           325           330           335
97 Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
98           340           345           350
100 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
101           355           360           365
103 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
104           370           375           380
106 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
107 385           390           395           400
109 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
110           405           410           415
112 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
113           420           425           430
115 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
116           435           440           445
118 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
119           450           455           460
121 Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile Gly Thr Asp Cys
122 465           470           475           480
124 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
125           485           490           495
127 Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
128           500           505           510
130 Val His Ser Gly
131           515
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 1548
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:

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140 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial base  
 141 sequence of human-originated soluble  
 142 thrombomodulin gene

144 &lt;400&gt; SEQUENCE: 2

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146 gcagagccgc agccgggtgg cagccagtgc gtcgagcacg actgcttcgc gctctacccg 120
147 ggccccgcga ccttcctcaa tgccagtcag atctgcgacg gactgcgggg ccacctaattg 180
148 acagtgcgct cctcggtggc tgccgatgtc atttccttgc tactgaacgg cgacggcggc 240
149 gttggccgcc ggcgccctctg gatcggcctg cagctgccac ccggctgcgg cgaccccaag 300
150 cgctcggggc ccctgcgcgg cttccagtgg gttacgggag acaacaacac cagctatagc 360
151 aggtgggcac ggctcgacct caatggggct cccctctgcg gcccggttgc cgctcgctgtc 420
152 tccgctgctg aggccactgt gcccgagcag ccgatctggg aggagcagca gtgcgaagtg 480
153 aaggccgatg gcttcctctg cgagttccac ttcccagcca cctgcaggcc actggctgtg 540
154 gagcccgccg ccgcgggtgc cgccgtctcg atcacctacg gcaccccggt cgcgggccgc 600
155 ggagcggact tccaggcgct gccgggtggc agctccgccc cggtggctcc cctcggttta 660
156 cagctaattg gcaccgcgcc gcccgagcgc gtccaggggg actgggcccag ggaggcgccg 720
157 ggcgcttggg actgcagcgt ggagaacggc ggctgcgagc acgcgtgcaa tgcgatccct 780
158 ggggctcccc gctgccagtg cccagccggc gccgccttgc aggcagacgg gcgctcctgc 840
159 accgcatccg cgacgcagtc ctgcaacgac ctctgcgagc atttctgcgt tcccaacccc 900
160 gaccagccgg gctcctactc gtgcatgtgc gagaccggct accggctggc ggccgaccaa 960
161 caccggtgcg aggacgtgga tgactgcata ctggagccca gtccgtgtcc gcagcgctgt 1020
162 gtcaacacac aggggtggctt cgagtgccac tgctacccta actacgacct ggtggacggc 1080
163 gagtgtgtgg agcccggtga cccgtgcttc agagccaact gcgagtacca gtgccagccc 1140
164 ctgaacaaaa ctagtacct ctgctcttgc gccgagggct tcgcgcccac tccccacgag 1200
165 ccgcacaggc gccagatggt ttgcaaccag actgcctgtc cagccgactg cgaccccaac 1260
166 acccaggcta gctgtgagtg ccctgaaggc tacatcctgg acgacgggtt catctgcacg 1320
167 gacatcgacg agtgcgaaaa cggcggtctt tgctccgggg tgtgccacaa cctccccggt 1380
168 accttcgagt gcatctgcgg gcccgactcg gcccttgtcc gccacattgg caccgactgt 1440
169 gactccggca aggtggacgg tggcgacagc ggctctggcg agcccccgcc cagcccgacg 1500
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173 &lt;210&gt; SEQ ID NO: 3

174 &lt;211&gt; LENGTH: 132

175 &lt;212&gt; TYPE: PRT

176 &lt;213&gt; ORGANISM: Artificial Sequence

178 &lt;220&gt; FEATURE:

179 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial amino  
 180 acid sequence of human-originated soluble  
 181 thrombomodulin

183 &lt;400&gt; SEQUENCE: 3

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184 Met Leu Gly Val Leu Val Leu Gly Ala Leu Ala Leu Ala Gly Leu Gly
185 1 5 10 15
187 Phe Pro Asp Pro Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro
188 20 25 30
190 Leu Asn Gln Thr Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro
191 35 40 45
193 Ile Pro His Glu Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala
194 50 55 60
196 Cys Pro Ala Asp Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro
197 65 70 75 80

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199 Glu Gly Tyr Ile Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu
200      85      90      95
202 Cys Glu Asn Gly Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly
203      100      105      110
205 Thr Phe Glu Cys Ile Cys Gly Pro Asp Ser Ala Leu Val Arg His Ile
206      115      120      125
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209      130
212 <210> SEQ ID NO: 4
213 <211> LENGTH: 396
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial base
219     sequence of human-originated soluble
220     thrombomodulin gene
222 <400> SEQUENCE: 4
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225 gtctgcgcgc agggcttcgc gccattccc cagagccgc acaggtgcca gatgttttgc 180
226 aaccagactg cctgtccagc cgactgcgac cccaacaccc aggctagctg tgagtgcctt 240
227 gaaggctaca tcttgacga cggtttcac tgcacggaca tcgacgagtg cgaaaacggc 300
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233 <211> LENGTH: 516
234 <212> TYPE: PRT
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial amino
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240     thrombomodulin
242 <400> SEQUENCE: 5
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246 Phe Pro Ala Pro Ala Glu Pro Gln Pro Gly Gly Ser Gln Cys Val Glu
247      20      25      30
249 His Asp Cys Phe Ala Leu Tyr Pro Gly Pro Ala Thr Phe Leu Asn Ala
250      35      40      45
252 Ser Gln Ile Cys Asp Gly Leu Arg Gly His Leu Met Thr Val Arg Ser
253      50      55      60
255 Ser Val Ala Ala Asp Val Ile Ser Leu Leu Leu Asn Gly Asp Gly Gly
256 65      70      75      80
258 Val Gly Arg Arg Arg Leu Trp Ile Gly Leu Gln Leu Pro Pro Gly Cys
259      85      90      95
261 Gly Asp Pro Lys Arg Leu Gly Pro Leu Arg Gly Phe Gln Trp Val Thr
262      100      105      110
264 Gly Asp Asn Asn Thr Ser Tyr Ser Arg Trp Ala Arg Leu Asp Leu Asn
265      115      120      125

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267 Gly Ala Pro Leu Cys Gly Pro Leu Cys Val Ala Val Ser Ala Ala Glu
268      130      135      140
270 Ala Thr Val Pro Ser Glu Pro Ile Trp Glu Glu Gln Gln Cys Glu Val
271 145      150      155      160
273 Lys Ala Asp Gly Phe Leu Cys Glu Phe His Phe Pro Ala Thr Cys Arg
274      165      170      175
276 Pro Leu Ala Val Glu Pro Gly Ala Ala Ala Ala Val Ser Ile Thr
277      180      185      190
279 Tyr Gly Thr Pro Phe Ala Ala Arg Gly Ala Asp Phe Gln Ala Leu Pro
280      195      200      205
282 Val Gly Ser Ser Ala Ala Val Ala Pro Leu Gly Leu Gln Leu Met Cys
283      210      215      220
285 Thr Ala Pro Pro Gly Ala Val Gln Gly His Trp Ala Arg Glu Ala Pro
286 225      230      235      240
288 Gly Ala Trp Asp Cys Ser Val Glu Asn Gly Gly Cys Glu His Ala Cys
289      245      250      255
291 Asn Ala Ile Pro Gly Ala Pro Arg Cys Gln Cys Pro Ala Gly Ala Ala
292      260      265      270
294 Leu Gln Ala Asp Gly Arg Ser Cys Thr Ala Ser Ala Thr Gln Ser Cys
295      275      280      285
297 Asn Asp Leu Cys Glu His Phe Cys Val Pro Asn Pro Asp Gln Pro Gly
298      290      295      300
300 Ser Tyr Ser Cys Met Cys Glu Thr Gly Tyr Arg Leu Ala Ala Asp Gln
301 305      310      315      320
303 His Arg Cys Glu Asp Val Asp Asp Cys Ile Leu Glu Pro Ser Pro Cys
304      325      330      335
306 Pro Gln Arg Cys Val Asn Thr Gln Gly Gly Phe Glu Cys His Cys Tyr
307      340      345      350
309 Pro Asn Tyr Asp Leu Val Asp Gly Glu Cys Val Glu Pro Val Asp Pro
310      355      360      365
312 Cys Phe Arg Ala Asn Cys Glu Tyr Gln Cys Gln Pro Leu Asn Gln Thr
313      370      375      380
315 Ser Tyr Leu Cys Val Cys Ala Glu Gly Phe Ala Pro Ile Pro His Glu
316 385      390      395      400
318 Pro His Arg Cys Gln Met Phe Cys Asn Gln Thr Ala Cys Pro Ala Asp
319      405      410      415
321 Cys Asp Pro Asn Thr Gln Ala Ser Cys Glu Cys Pro Glu Gly Tyr Ile
322      420      425      430
324 Leu Asp Asp Gly Phe Ile Cys Thr Asp Ile Asp Glu Cys Glu Asn Gly
325      435      440      445
327 Gly Phe Cys Ser Gly Val Cys His Asn Leu Pro Gly Thr Phe Glu Cys
328      450      455      460
330 Ile Cys Gly Pro Asp Ser Ala Leu Ala Arg His Ile Gly Thr Asp Cys
331 465      470      475      480
333 Asp Ser Gly Lys Val Asp Gly Gly Asp Ser Gly Ser Gly Glu Pro Pro
334      485      490      495
336 Pro Ser Pro Thr Pro Gly Ser Thr Leu Thr Pro Pro Ala Val Gly Leu
337      500      505      510
339 Val His Ser Gly

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**VERIFICATION SUMMARY**

DATE: 11/10/2005

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